

## Sheet 1 of 6

FIG. 1A-1

Mtt1	793	.....SQIFTTNIAAGGR <sup>+</sup> EIKV <sup>-</sup> K E.....CP
Upf1	547	.....ADVCCCTCVGAGDKRIDT...K.....FR
Sen1	1413	DRDEMREKNSVNYRNRDLDRRNAQAHILAVSDIICSTLGS <sup>+</sup> AHDVLA <sup>+</sup> TMGIK.....FD
Dip1	351	.....FKTIKDLIQSRIVVTLHGSSSRRELCSLYRDDDPNFQLFD
Dna2	1128	KHKVHPDTQKYVPNPYASVKSYNDYLSKINSTSVATTCIGI.NDIIFTLNED.....FD
consensus	241	1 s iv tT ig q r Lti k fd

Mt1	816	VIMDEATQSSSEASTLVPLSLPCIR..NFVFGDEKQLSFSNIP.....QLE
Upf1	568	TVIIDESTQASEPECLIPF.VKGAK..QVTLVGDHQQLG....PVILERKAADA..GLK
Sen1	1467	TVIIDEACQCTELSSIIPIRY.GGK..RCIMVGDPNQL....PPTVLSGAASNF..KYN
Dip1	391	TVIIDEVSQAMEPQCWIPIAHQNFHKLVLADGNKQL....PPTIKTEDDKNVIHNL
Dna2	1182	TVIIDEASQISMPVALGPLRY....GNRFIMVGDHYQL....PPLVKNDAAAR..LGGLE
consensus	301	tviidEaTQ sep liPl g r x ilvGD QL pPi a le

Mtt1	862	TSLEFRLVSLNGTYKNPLM..LDTQYRMHFKISEFFLKKIYNCEL
Upf1	618	QSLFERLISLGHV..PIR.LEVQYRMNFYLSEFPSNMFEYEGSL
Sen1	1517	QSLFVRMEKN...SSPYL.LDVQYRMHESISKFFPSSEFYQGRIL
Dip1	446	TLFDRIIKIFPKRDMVKELNVQYRMNQKIMEFFPSHSMYNGKILLADATVANRLLDLPV
Dna2	1231	ESLEKTFCEKHPS..VAELTIQYRMCGDIUTLSNFLIYDNKIKCGNNEVFAQSLELPM
consensus	361	sLFervl pl LdvQYRM p isefps iYngRL

Mtt1	904	.....
Upf1	658	.....
Sen1	1556	.....
Dip1	506	DA.....
Dna2	1289	EALSRYNESANSKQWLEDILEPTRKVVFLNYDNCPDIIIEQSEKDNITNHGEAELTLQCV
consensus	421	

## Sheet 2 of 6

FIG. 1B

Mtt1	904	.....KDGVTDEQKA.....	WPGVQH.....	PLFFYQCDLGHESR	
Upf1	658	.....QNGVTIEQRTVPNSKFPPIRGI		PMFW.ANYGRE..	
Sen1	1556	.....KDG.....	PGMDILNKRPHWQLEPLAPYKFFDIISGRQ..		
Dip1	508	.....TPSED.....	DDDTKIPLIWD.TQGDFFQ		
Dna2	1349	EGMLLSGVPCED.....			
consensus	481	dg	p	pl fy	g e
Mtt1	934	VRSTQRDIVGFTYE.....	NKHECVEIVKIIQIILMLDKKVPLE...EI		
Upf1	692	...EISANGTSFL.....	NRIEAMNCERIIITKILFRDGVKP.E...QI		
Sen1	1589	...EQNAKTMSYT.....	NMEIRVAIELVDYLFRKFDNKIDFTGKI		
Dip1	532	ETADEATILGSKYNEGEIAIVKEHIENLRSENVPE		NSI	
Dna2	1361	.....		I	
consensus	541	e g ty	n e	ii l	e l
Mtt1	974	GVITPYSACQRDILSDILTKNVVINPKQISMQQEYDEIELFNAAGSQGTAGSLQNNVINII			
Upf1	727	GVITPYEGQRAYILOYMOMN.....	GSIDK...DLY		
Sen1	1628	GIISPYREQ.....	MQMRKEFARYFGGMINKS.....		
Dip1	570	GVI SPYNAQVSHLKKLIHDELKLTID.....			
Dna2	1362	GVTILYRAQLRIILKKIFNKIV.....			Y
consensus	601	Gvitpy aQ l il nv			g l
Mtt1	1034	NGLHVATVDSEFGHEKSEFIIFSCVRN.NTENKIGFIIDKRRINVALTRAK~			
Upf1	755	IKVEVASVDAFQGREKDYIILSCVRA.NEQQAIGFIIDERRLNVALTRAK~			
Sen1	1656	..IDENIIDCFQCGQKEIILISCVRADDTKSSVGFKDFRRINVALTRAK~			
Dip1	595	..IEISTVDGFQGREKDYIILSVRS.NEKFEVGFLEERRLNVALTRPR~			
Dna2	1384	DGLEILTADQFGQDKKCIILISMVRRNSQLNGGAILLEIRHVNVALTRAKS			
consensus	661	lev tvDaFQGreKd iilScvR n n igfLkd RRINValTrak			